

(1) GENERAL INFORMATION:

- (2) INFORMATION FOR SEQ ID NO:1:

- (ii) MOLECULE TYPE: cDNA

- ```
(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 49..1341
 (C) IDENTIFICATION METHOD: experimental
 (D) OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
product= "Op1"
evidence= EXPERIMENTAL
standard_name= "Op1"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|       |       |       |       |       |       |       |       |       |      |     |     |     |     |     |     |     |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|------|-----|-----|-----|-----|-----|-----|-----|
| GGTGC | GGGCC | CGGAG | CCCGG | AGCCC | GGGTA | GCGCG | TAGAG | CCGCG | CGCG | ATG | CAC | GTG | 57  |     |     |     |
|       |       |       |       |       |       |       |       |       |      | Met | His | Val |     |     |     |     |
|       |       |       |       |       |       |       |       |       |      | 1   |     |     |     |     |     |     |
| CGC   | TCA   | CTG   | CGA   | GCT   | GCG   | GCG   | CCG   | CAC   | AGC  | TTC | GTG | GCG | CTC | TGG | GCA | 105 |
| Arg   | Ser   | Leu   | Arg   | Ala   | Ala   | Ala   | Pro   | His   | Ser  | Phe | Val | Ala | Leu | Trp | Ala |     |
|       | 5     |       |       |       |       | 10    |       |       |      |     | 15  |     |     |     |     |     |
| CCC   | CTG   | TTC   | CTG   | CTG   | CGC   | TCC   | GCC   | CTG   | GCC  | GAC | TTC | AGC | CTG | GAC | AAC | 153 |
| Pro   | Leu   | Phe   | Leu   | Leu   | Arg   | Ser   | Ala   | Leu   | Ala  | Asp | Phe | Ser | Leu | Asp | Asn |     |
| 20    |       |       |       |       | 25    |       |       |       |      | 30  |     |     |     |     | 35  |     |
| GAG   | GTG   | CAC   | TCG   | AGC   | TTC   | ATC   | CAC   | CGG   | CGC  | CTC | CGC | AGC | CAG | GAG | CGG | 201 |
| Glu   | Val   | His   | Ser   | Ser   | Phe   | Ile   | His   | Arg   | Arg  | Leu | Arg | Ser | Gln | Glu | Arg |     |
|       |       |       |       | 40    |       |       |       |       | 45   |     |     |     |     | 50  |     |     |
| CGG   | GAG   | ATG   | CAG   | CGC   | GAG   | ATC   | CTC   | TCC   | ATT  | TTG | GGC | TTG | CCC | CAC | CGC | 249 |
| Arg   | Glu   | Met   | Gln   | Arg   | Glu   | Ile   | Leu   | Ser   | Ile  | Leu | Gly | Leu | Pro | His | Arg |     |
|       |       |       | 55    |       |       |       |       | 60    |      |     |     |     | 65  |     |     |     |
| CCG   | CGC   | CCG   | CAC   | CTC   | CAG   | GGC   | AAG   | CAC   | AAC  | TCG | GCA | CCC | ATG | TTC | ATG | 297 |
| Pro   | Arg   | Pro   | His   | Leu   | Gln   | Gly   | Lys   | His   | Asn  | Ser | Ala | Pro | Met | Phe | Met |     |
|       |       | 70    |       |       |       |       | 75    |       |      |     |     | 80  |     |     |     |     |
| CTG   | GAC   | CTG   | TAC   | AAC   | GCC   | ATG   | GCG   | GTG   | GAG  | GAG | GGC | GGC | GGG | CCC | GGC | 345 |
| Leu   | Asp   | Leu   | Tyr   | Asn   | Ala   | Met   | Ala   | Val   | Glu  | Glu | Gly | Gly | Gly | Pro | Gly |     |
|       | 85    |       |       |       |       | 90    |       |       |      |     | 95  |     |     |     |     |     |
| GGC   | CAG   | GGC   | TTC   | TCC   | TAC   | CCC   | TAC   | AAG   | GCC  | GTC | TTC | AGT | ACC | CAG | GGC | 393 |
| Gly   | Gln   | Gly   | Phe   | Ser   | Tyr   | Pro   | Tyr   | Lys   | Ala  | Val | Phe | Ser | Thr | Gln | Gly |     |
| 100   |       |       |       |       | 105   |       |       |       |      | 110 |     |     |     |     | 115 |     |
| CCC   | CCT   | CTG   | GCC   | AGC   | CTG   | CAA   | GAT   | AGC   | CAT  | TTC | CTC | ACC | GAC | GCC | GAC | 441 |
| Pro   | Pro   | Leu   | Ala   | Ser   | Leu   | Gln   | Asp   | Ser   | His  | Phe | Leu | Thr | Asp | Ala | Asp |     |
|       |       |       |       | 120   |       |       |       |       | 125  |     |     |     |     | 130 |     |     |
| ATG   | GTC   | ATG   | AGC   | TTC   | GTC   | AAC   | CTC   | GTG   | GAA  | CAT | GAC | AAG | GAA | TTC | TTC | 489 |
| Met   | Val   | Met   | Ser   | Phe   | Val   | Asn   | Leu   | Val   | Glu  | His | Asp | Lys | Glu | Phe | Phe |     |
|       |       |       | 135   |       |       |       |       | 140   |      |     |     | 145 |     |     |     |     |
| CAC   | CCA   | CGC   | TAC   | CAC   | CAT   | CGA   | GAG   | TTC   | CGG  | TTT | GAT | CTT | TCC | AAG | ATC | 537 |
| His   | Pro   | Arg   | Tyr   | His   | His   | Arg   | Glu   | Phe   | Arg  | Phe | Asp | Leu | Ser | Lys | Ile |     |
|       |       | 150   |       |       |       |       | 155   |       |      |     |     | 160 |     |     |     |     |
| CCA   | GAA   | GGG   | GAA   | GCT   | GTC   | ACG   | GCA   | GCC   | GAA  | TTC | CGG | ATC | TAC | AAG | GAC | 585 |
| Pro   | Glu   | Gly   | Glu   | Ala   | Val   | Thr   | Ala   | Ala   | Glu  | Phe | Arg | Ile | Tyr | Lys | Asp |     |
|       | 165   |       |       |       |       | 170   |       |       |      |     | 175 |     |     |     |     |     |
| TAC   | ATC   | CGG   | GAA   | CGC   | TTC   | GAC   | AAT   | GAG   | ACG  | TTC | CGG | ATC | AGC | GTT | TAT | 633 |
| Tyr   | Ile   | Arg   | Glu   | Arg   | Phe   | Asp   | Asn   | Glu   | Thr  | Phe | Arg | Ile | Ser | Val | Tyr |     |
| 180   |       |       |       |       | 185   |       |       |       |      | 190 |     |     |     |     | 195 |     |
| CAG   | GTG   | CTC   | CAG   | GAG   | CAC   | TTG   | GGC   | AGG   | GAA  | TCG | GAT | CTC | TTC | CTG | CTC | 681 |
| Gln   | Val   | Leu   | Gln   | Glu   | His   | Leu   | Gly   | Arg   | Glu  | Ser | Asp | Leu | Phe | Leu | Leu |     |
|       |       |       |       | 200   |       |       |       |       | 205  |     |     |     |     | 210 |     |     |
| GAC   | AGC   | CGT   | ACC   | CTC   | TGG   | GCC   | TCG   | GAG   | GAG  | GGC | TGG | CTG | GTG | TTT | GAC | 729 |
| Asp   | Ser   | Arg   | Thr   | Leu   | Trp   | Ala   | Ser   | Glu   | Glu  | Gly | Trp | Leu | Val | Phe | Asp |     |
|       |       |       | 215   |       |       |       |       | 220   |      |     |     |     | 225 |     |     |     |
| ATC   | ACA   | GCC   | ACC   | AGC   | AAC   | CAC   | TGG   | GTG   | GTC  | AAT | CCG | CGG | CAC | AAC | CTG | 777 |
| Ile   | Thr   | Ala   | Thr   | Ser   | Asn   | His   | Trp   | Val   | Val  | Asn | Pro | Arg | His | Asn | Leu |     |
|       |       | 230   |       |       |       |       | 235   |       |      |     |     | 240 |     |     |     |     |
| GGC   | CTG   | CAG   | CTC   | TCG   | GTG   | GAG   | ACG   | CTG   | GAT  | GGG | CAG | AGC | ATC | AAC | CCC | 825 |
| Gly   | Leu   | Gln   | Leu   | Ser   | Val   | Glu   | Thr   | Leu   | Asp  | Gly | Gln | Ser | Ile | Asn | Pro |     |
|       | 245   |       |       |       |       | 250   |       |       |      |     | 255 |     |     |     |     |     |

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|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| AAG TTG GCG GGC CTG ATT GGG CGG CAC GGG CCC CAG AAC AAG CAG CCC<br>Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro<br>260 265 270 275 | 873  |
| TTC ATG GTG GCT TTC TTC AAG GCC ACG GAG GTC CAC TTC CGC AGC ATC<br>Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile<br>280 285 290     | 921  |
| CGG TCC ACG GGG AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG AGC CCC<br>Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro<br>295 300 305     | 969  |
| AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC GTG GCA GAG AAC AGC AGC<br>Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser<br>310 315 320     | 1017 |
| AGC GAC CAG AGG CAG GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC<br>Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe<br>325 330 335     | 1065 |
| CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG CCT GAA GGC TAC GCC<br>Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala<br>340 345 350 355 | 1113 |
| GCC TAC TAC TGT GAG GGG GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG<br>Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met<br>360 365 370     | 1161 |
| AAC GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC CAC TTC ATC AAC<br>Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn<br>375 380 385     | 1209 |
| CCG GAA ACG GTG CCC AAG CCC TGC TGT GCG CCC ACG CAG CTC AAT GCC<br>Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala<br>390 395 400     | 1257 |
| ATC TCC GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC CTG AAG AAA<br>Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys<br>405 410 415     | 1305 |
| TAC AGA AAC ATG GTG GTC CGG GCC TGT GGC TGC CAC TAGCTCCTCC<br>Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His<br>420 425 430                          | 1351 |
| GAGAATTCAG ACCCTTTGGG GCCAAGTTTT TCTGGATCCT CCATTGCTCG CCTTGGCCAG                                                                                     | 1411 |
| GAACCAGCAG ACCAACTGCC TTTTGTGAGA CCTTCCCCTC CCTATCCCCA ACTTTAAAGG                                                                                     | 1471 |
| TGTGAGAGTA TTAGGAAACA TGAGCAGCAT ATGGCTTTTG ATCAGTTTTT CAGTGGCAGC                                                                                     | 1531 |
| ATCCAATGAA CAAGATCCTA CAAGCTGTGC AGGCAAAACC TAGCAGGAAA AAAAAACAAC                                                                                     | 1591 |
| GCATAAAGAA AAATGGCCGG GCCAGGTCAT TGGCTGGGAA GTCTCAGCCA TGCACGGACT                                                                                     | 1651 |
| CGTTTCCAGA_GGTAATTATG AGCGCCTACC AGCCAGGCCA CCCAGCCGTG GGAGGAAGGG                                                                                     | 1711 |
| GGCGTGGCAA GGGGTGGGCA CATTGGTGTC TGTGCGAAAG GAAAATTGAC CCGGAAGTTC                                                                                     | 1771 |
| CTGTAATAAA TGTCACAATA AAACGAATGA ATGAAAAAAA AAAAAAAAAA A                                                                                              | 1822 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 431 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | His | Val | Arg | Ser | Leu | Arg | Ala | Ala | Ala | Pro | His | Ser | Phe | Val | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Trp | Ala | Pro | Leu | Phe | Leu | Leu | Arg | Ser | Ala | Leu | Ala | Asp | Phe | Ser |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Leu | Asp | Asn | Glu | Val | His | Ser | Ser | Phe | Ile | His | Arg | Arg | Leu | Arg | Ser |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gln | Glu | Arg | Arg | Glu | Met | Gln | Arg | Glu | Ile | Leu | Ser | Ile | Leu | Gly | Leu |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Pro | His | Arg | Pro | Arg | Pro | His | Leu | Gln | Gly | Lys | His | Asn | Ser | Ala | Pro |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Met | Phe | Met | Leu | Asp | Leu | Tyr | Asn | Ala | Met | Ala | Val | Glu | Glu | Gly | Gly |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Gly | Pro | Gly | Gly | Gln | Gly | Phe | Ser | Tyr | Pro | Tyr | Lys | Ala | Val | Phe | Ser |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Thr | Gln | Gly | Pro | Pro | Leu | Ala | Ser | Leu | Gln | Asp | Ser | His | Phe | Leu | Thr |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Asp | Ala | Asp | Met | Val | Met | Ser | Phe | Val | Asn | Leu | Val | Glu | His | Asp | Lys |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Glu | Phe | Phe | His | Pro | Arg | Tyr | His | His | Arg | Glu | Phe | Arg | Phe | Asp | Leu |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Ser | Lys | Ile | Pro | Glu | Gly | Glu | Ala | Val | Thr | Ala | Ala | Glu | Phe | Arg | Ile |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Tyr | Lys | Asp | Tyr | Ile | Arg | Glu | Arg | Phe | Asp | Asn | Glu | Thr | Phe | Arg | Ile |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Ser | Val | Tyr | Gln | Val | Leu | Gln | Glu | His | Leu | Gly | Arg | Glu | Ser | Asp | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Phe | Leu | Leu | Asp | Ser | Arg | Thr | Leu | Trp | Ala | Ser | Glu | Glu | Gly | Trp | Leu |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Val | Phe | Asp | Ile | Thr | Ala | Thr | Ser | Asn | His | Trp | Val | Val | Asn | Pro | Arg |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| His | Asn | Leu | Gly | Leu | Gln | Leu | Ser | Val | Glu | Thr | Leu | Asp | Gly | Gln | Ser |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ile | Asn | Pro | Lys | Leu | Ala | Gly | Leu | Ile | Gly | Arg | His | Gly | Pro | Gln | Asn |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Lys | Gln | Pro | Phe | Met | Val | Ala | Phe | Phe | Lys | Ala | Thr | Glu | Val | His | Phe |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Ser | Ile | Arg | Ser | Thr | Gly | Ser | Lys | Gln | Arg | Ser | Gln | Asn | Arg | Ser |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Lys | Thr | Pro | Lys | Asn | Gln | Glu | Ala | Leu | Arg | Met | Ala | Asn | Val | Ala | Glu |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Asn | Ser | Ser | Ser | Asp | Gln | Arg | Gln | Ala | Cys | Lys | Lys | His | Glu | Leu | Tyr |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Val | Ser | Phe | Arg | Asp | Leu | Gly |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:3:

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

(2) INFORMATION FOR SEQ ID NO:4:

(ii) MOLECULE TYPE: protein

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(ix) FEATURE:
 (A) NAME/KEY: Protein
 (B) LOCATION: 1..97
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(2) INFORMATION FOR SEQ ID NO:5:

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: Protein

(B) LOCATION: 1..102

(D) OTHER INFORMATION: /label= Generic-Seq-8

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/NOTE= "wherein each Xaa is independently selected from a group
of one or more specified amino acids as defined in the
specification."

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|           |           |           |           |          |           |           |     |           |           |           |           |     |           |           |           |  |
|-----------|-----------|-----------|-----------|----------|-----------|-----------|-----|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|--|
| Cys<br>1  | Xaa       | Xaa       | Xaa       | Xaa<br>5 | Leu       | Xaa       | Xaa | Xaa       | Phe<br>10 | Xaa       | Xaa       | Xaa | Gly       | Trp<br>15 | Xaa       |  |
| Xaa       | Xaa       | Xaa       | Xaa<br>20 | Xaa      | Pro       | Xaa       | Xaa | Xaa<br>25 | Xaa       | Ala       | Xaa       | Tyr | Cys<br>30 | Xaa       | Gly       |  |
| Xaa       | Cys       | Xaa<br>35 | Xaa       | Pro      | Xaa       | Xaa<br>40 | Xaa | Xaa       | Xaa       | Xaa       | Xaa<br>45 | Asn | His       | Ala       |           |  |
| Xaa       | Xaa<br>50 | Xaa       | Xaa       | Xaa      | Xaa       | Xaa<br>55 | Xaa | Xaa       | Xaa       | Xaa       | Xaa<br>60 | Xaa | Xaa       | Xaa       | Xaa       |  |
| Xaa<br>65 | Cys       | Cys       | Xaa       | Pro      | Xaa<br>70 | Xaa       | Xaa | Xaa       | Xaa       | Xaa<br>75 | Xaa       | Xaa | Leu       | Xaa       | Xaa<br>80 |  |
| Xaa       | Xaa       | Xaa       | Xaa<br>85 | Val      | Xaa       | Leu       | Xaa | Xaa<br>90 | Xaa       | Xaa       | Xaa       | Met | Xaa<br>95 | Val       |           |  |

Xaa Xaa Cys Xaa Cys Xaa  
100

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 97 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein  
(B) LOCATION: 1..97  
(D) OTHER INFORMATION: /label= Generic-Seq-9

/note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15  
Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly Xaa Cys Xaa Xaa Xaa  
20 25 30  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Pro  
50 55 60  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
65 70 75 80  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys  
85 90 95  
Xaa

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: Protein  
(B) LOCATION: 1..102  
(D) OTHER INFORMATION: /label= Generic-Seq-10

/note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
1 5 10 15

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Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Gly  
20 25 30  
Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40 45  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
50 55 60  
Xaa Xaa Cys Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
65 70 75 80  
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
85 90 95  
Xaa Xaa Cys Xaa Cys Xaa  
100

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Cys Xaa Xaa Xaa Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Protein
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /note= "wherein each Xaa is independently selected from a group of one or more specified amino acids as defined in the specification"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Cys Xaa Xaa Xaa Xaa  
1 5

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